

# Sequence Listing

<110> ASHKENAZI, AVI J  
 BOTSTEIN, DAVID  
 DODGE, KELLY H.  
 GURNEY, AUSTIN L.  
 KIM, KYUNG JIN  
 LAWRENCE, DAVID A.  
 PITTI, ROBERT  
 ROY, MARGARET A  
 TUMAS, DANIEL B  
 WOOD, WILLIAM I.

<120> DcR3 Polypeptide, A TNFR Homolog

<130> P1134R2 REVISED

<140> US 09/157,289

<141> 1998-09-18

<150> US 60/059,288

<151> 1997-09-18

<150> US 60/094,640

<151> 1998-07-30

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<212> PRT

<213> Homo sapiens

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Ala	Glu	Thr	Pro	Thr	Tyr	Pro	Trp	Arg	Asp	Ala	Glu	Thr	Gly	Glu
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Arg	Leu	Val	Cys	Ala	Gln	Cys	Pro	Pro	Gly	Thr	Phe	Val	Gln	Arg
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Pro	Cys	Arg	Arg	Asp	Ser	Pro	Thr	Thr	Cys	Gly	Pro	Cys	Pro	Pro
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Arg	His	Tyr	Thr	Gln	Phe	Trp	Asn	Tyr	Leu	Glu	Arg	Cys	Arg	Tyr
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Cys	Asn	Val	Leu	Cys	Gly	Glu	Arg	Glu	Glu	Glu	Ala	Arg	Ala	Cys
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His	Ala	Thr	His	Asn	Arg	Ala	Cys	Arg	Cys	Arg	Thr	Gly	Phe	Phe
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Ala	His	Ala	Gly	Phe	Cys	Leu	Glu	His	Ala	Ser	Cys	Pro	Pro	Gly
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Ala	Gly	Val	Ile	Ala	Pro	Gly	Thr	Pro	Ser	Gln	Asn	Thr	Gln	Cys
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Gln	Pro	Cys	Pro	Pro	Gly	Thr	Phe	Ser	Ala	Ser	Ser	Ser	Ser	Ser
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Glu	Gln	Cys	Gln	Pro	His	Arg	Asn	Cys	Thr	Ala	Leu	Gly	Leu	Ala
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Leu	Asn	Val	Pro	Gly	Ser	Ser	Ser	His	Asp	Thr	Leu	Cys	Thr	Ser
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				200					205					210
Cys	Glu	Arg	Ala	Val	Ile	Asp	Phe	Val	Ala	Phe	Gln	Asp	Ile	Ser
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Ile	Lys	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala	Leu	Glu	Ala	Pro	Glu
				230					235					240
Gly	Trp	Gly	Pro	Thr	Pro	Arg	Ala	Gly	Arg	Ala	Ala	Leu	Gln	Leu
				245					250					255
Lys	Leu	Arg	Arg	Arg	Leu	Thr	Glu	Leu	Leu	Gly	Ala	Gln	Asp	Gly
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Ala	Leu	Leu	Val	Arg	Leu	Leu	Gln	Ala	Leu	Arg	Val	Ala	Arg	Met
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Pro	Gly	Leu	Glu	Arg	Ser	Val	Arg	Glu	Arg	Phe	Leu	Pro	Val	His
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atgagggcgc tggagggggc aggcctgtcg ctgctgtgcc tgggtgttggc 150  
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ggagcgtgag gaggaggcac gggcttgcca cgccaccac aaccgtgcct 150  
gccgctgccg caccggcttc ttgcgcacg ctggtttctg cttggagcac 200  
gcatcgtgtc cacctggtgc cggcgtgatt gccccgggca ccccaagcca 250  
gaacacgcag tgcctagccg tgccccccag gcaccttctc agccagcagc 300  
tccagctcag agcagtgcc accccaccgc aactgcacgg ccctgggcct 350  
ggccctcaat gtgccaggct ctctctccca tgacaccctg tgcaccagct 400  
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cgtgccgtca tcgactttgt ggctttccag gacatctcca t 491

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<213> Unknown

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cattctggaa ctacctggag cgc 73

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cgcatacgtgt ccacctgggtg ccggcgtgat tncctccgggc acccccagcc 200

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cttcctcct ggctgcaggc acccccagcc agaacacgca gnccagcgt 150  
gccccccagg caccttctca gccagcagct ccagctcaga gcagtgccag 200  
ccccaccgca actgcacggc cctgggcctg gccctcaatg tgccaggctc 250  
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 aggtctttcc tcccatgaca cgctgtgcac cagctgcact ggcttcccc 150  
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 atgtgccagg ctcttctctc catgacaccc tgtgcaccag ctgcactggc 200  
 ttccccctca gcaccagggg accaggagct gaggagtgtg agcgtgccgt 250  
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35 40 45  
Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly  
50 55 60  
Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys  
65 70 75  
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80 85 90  
Pro Glu Cys Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val  
95 100 105  
Glu Thr Gln Ala Cys Thr Arg Glu Gln Asn Arg Ile Cys Thr Cys  
110 115 120  
Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln Glu Gly Cys Arg  
125 130 135  
Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val Ala  
140 145 150  
Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala  
155 160 165  
Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg  
170 175 180  
Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly Asn Ala Ser  
185 190 195  
Arg Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser Met Ala  
200 205 210

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Pro Gly Ala Val	His Leu Pro Gln Pro	Val Ser Thr Arg Ser	Gln
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His Thr Gln Pro	Thr Pro Glu Pro Ser	Thr Ala Pro Ser Thr	Ser
	230	235	240
Phe Leu Leu Pro	Met Gly Pro Ser Pro	Pro Ala Glu Gly Ser	Thr
	245	250	255
Gly Asp Phe Ala	Leu Pro Val Gly Leu	Ile Val Gly Val Thr	Ala
	260	265	270
Leu Gly Leu Leu	Ile Ile Gly Val Val	Asn Cys Val Ile Met	Thr
	275	280	285
Gln Val Lys Lys	Lys Pro Leu Cys Leu	Gln Arg Glu Ala Lys	Val
	290	295	300
Pro His Leu Pro	Ala Asp Lys Ala Arg	Gly Thr Gln Gly Pro	Glu
	305	310	315
Gln Gln His Leu	Leu Ile Thr Ala Pro	Ser Ser Ser Ser Ser	Ser
	320	325	330
Leu Glu Ser Ser	Ala Ser Ala Leu Asp	Arg Arg Ala Pro Thr	Arg
	335	340	345
Asn Gln Pro Gln	Ala Pro Gly Val Glu	Ala Ser Gly Ala Gly	Glu
	350	355	360
Ala Arg Ala Ser	Thr Gly Ser Ser Asp	Ser Ser Pro Gly Gly	His
	365	370	375
Gly Thr Gln Val	Asn Val Thr Cys Ile	Val Asn Val Cys Ser	Ser
	380	385	390
Ser Asp His Ser	Ser Gln Cys Ser Ser	Gln Ala Ser Ser Thr	Met
	395	400	405
Gly Asp Thr Asp	Ser Ser Pro Ser Glu	Ser Pro Lys Asp Glu	Gln
	410	415	420
Val Pro Phe Ser	Lys Glu Glu Cys Ala	Phe Arg Ser Gln Leu	Glu
	425	430	435
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 Tyr Asp Glu Glu Thr Ser His Gln Leu Leu Cys Asp Lys Cys Pro  
 35 40 45  
 Pro Gly Thr Tyr Leu Lys Gln His Cys Thr Ala Lys Trp Lys Thr  
 50 55 60  
 Val Cys Ala Pro Cys Pro Asp His Tyr Tyr Thr Asp Ser Trp His  
 65 70 75  
 Thr Ser Asp Glu Cys Leu Tyr Cys Ser Pro Val Cys Lys Glu Leu  
 80 85 90  
 Gln Tyr Val Lys Gln Glu Cys Asn Arg Thr His Asn Arg Val Cys  
 95 100 105  
 Glu Cys Lys Glu Gly Arg Tyr Leu Glu Ile Glu Phe Cys Leu Lys  
 110 115 120  
 His Arg Ser Cys Pro Pro Gly Phe Gly Val Val Gln Ala Gly Thr  
 125 130 135  
 Pro Glu Arg Asn Thr Val Cys Lys Arg Cys Pro Asp Gly Phe Phe  
 140 145 150  
 Ser Asn Glu Thr Ser Ser Lys Ala Pro Cys Arg Lys His Thr Asn  
 155 160 165  
 Cys Ser Val Phe Gly Leu Leu Leu Thr Gln Lys Gly Asn Ala Thr  
 170 175 180  
 His Asp Asn Ile Cys Ser Gly Asn Ser Glu Ser Thr Gln Lys Cys  
 185 190 195  
 Gly Ile Asp Val Thr Leu Cys Glu Glu Ala Phe Phe Arg Phe Ala  
 200 205 210  
 Val Pro Thr Lys Phe Thr Pro Asn Trp Leu Ser Val Leu Val Asp  
 215 220 225

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Asn Leu Pro Gly Thr Lys Val Asn Ala Glu Ser Val Glu Arg Ile  
 230 235 240

Lys Arg Gln His Ser Ser Gln Glu Gln Thr Phe Gln Leu Leu Lys  
 245 250 255

Leu Trp Lys His Gln Asn Lys Ala Gln Asp Ile Val Lys Lys Ile  
 260 265 270

Ile Gln Asp Ile Asp Leu Cys Glu Asn Ser Val Gln Arg His Ile  
 275 280 285

Gly His Ala Asn Leu Thr Phe Glu  
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